

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/256,631DATE: 07/06/95
TIME: 11:50:51

INPUT SET: S4634.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

H/O

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Lobb, Roy R.

(ii) TITLE OF INVENTION: Treatment for Asthma

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD

(B) STREET: 60 State Street, Suite 510

(C) CITY: Boston

(D) STATE: Massachusetts

(E) COUNTRY: USA

(F) ZIP: 02109-1875

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/256,631

(B) FILING DATE: 12-JUL-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US93/00030

(B) FILING DATE: 12-JAN-1993

(C) APPLICATION NUMBER: US 07/821,768

(D) FILING DATE: 13-JAN-1992

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Myers, Louis (PLM)

(B) REGISTRATION NUMBER: 35,965

(C) REFERENCE/DOCKET NUMBER: D002 CIP PCT (BGP-021US)

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617)227-7400

(B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

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47      (i) SEQUENCE CHARACTERISTICS:
48          (A) LENGTH: 360 base pairs
49          (B) TYPE: nucleic acid
50          (C) STRANDEDNESS: single
51          (D) TOPOLOGY: linear
52
53      (ii) MOLECULE TYPE: cDNA
54
55
56      (ix) FEATURE:
57          (A) NAME/KEY: CDS
58          (B) LOCATION: 1..360
59
60      (ix) FEATURE:
61          (A) NAME/KEY: misc_feature
62          (B) LOCATION: 1
63          (D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy
64              chain variable region; amino acid 1 is Glu (E) but
65              Gln (Q) may be substituted"
66
67
68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70      GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA      48
71      Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
72      1          5          10          15
73
74      GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT      96
75      Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
76      20          25          30
77
78      ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA      144
79      Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
80      35          40          45
81
82      AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG      192
83      Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
84      50          55          60
85
86      GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG      240
87      Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
88      65          70          75          80
89
90      CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA      288
91      Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
92      85          90          95
93
94      GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA      336
95      Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
96      100          105          110
97
98      GGG ACC ACG GTC ACC GTC TCC TCA      360
99      Gly Thr Thr Val Thr Val Ser Ser
  
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100 115 120
101
102
103 (2) INFORMATION FOR SEQ ID NO:2:
104
105 (i) SEQUENCE CHARACTERISTICS:
106 (A) LENGTH: 120 amino acids
107 (B) TYPE: amino acid
108 (D) TOPOLOGY: linear
109
110 (ii) MOLECULE TYPE: protein
111
112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
113
114 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
115 1 5 10 15
116
117 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
118 20 25 30
119
120 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
121 35 40 45
122
123 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
124 50 55 60
125
126 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
127 65 70 75 80
128
129 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
130 85 90 95
131
132 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
133 100 105 110
134
135 Gly Thr Thr Val Thr Val Ser Ser
136 115 120
137
138 (2) INFORMATION FOR SEQ ID NO:3:
139
140 (i) SEQUENCE CHARACTERISTICS:
141 (A) LENGTH: 318 base pairs
142 (B) TYPE: nucleic acid
143 (C) STRANDEDNESS: single
144 (D) TOPOLOGY: linear
145
146 (ii) MOLECULE TYPE: cDNA
147
148
149 (ix) FEATURE:
150 (A) NAME/KEY: CDS
151 (B) LOCATION: 1..318
152 (D) OTHER INFORMATION: /note= "HP1/2 light chain variable"

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153 region"

154

155 (ix) FEATURE:

156 (A) NAME/KEY: misc_feature

157 (B) LOCATION: 1

158 (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light
159 chain variable region"

160

161

162 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

163

164	AGT	ATT	GTG	ATG	ACC	CAG	ACT	CCC	AAA	TTC	CTG	CTT	GTT	TCA	GCA	GGA	48
165	Ser	Ile	Val	Met	Thr	Gln	Thr	Pro	Lys	Phe	Leu	Leu	Val	Ser	Ala	Gly	
166	1				5					10					15		

167

168	GAC	AGG	GTT	ACC	ATA	ACC	TGC	AAG	GCC	AGT	CAG	AGT	GTG	ACT	AAT	GAT	96
169	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Thr	Asn	Asp	
170				20					25					30			

171

172	GTA	GCT	TGG	TAC	CAA	CAG	AAG	CCA	GGG	CAG	TCT	CCT	AAA	CTG	CTG	ATA	144
173	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	
174			35					40					45				

175

176	TAT	TAT	GCA	TCC	AAT	CGC	TAC	ACT	GGA	GTC	CCT	GAT	CGC	TTC	ACT	GGC	192
177	Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	
178		50					55				60						

179

180	AGT	GGA	TAT	GGG	ACG	GAT	TTC	ACT	TTC	ACC	ATC	AGC	ACT	GTG	CAG	GCT	240
181	Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Thr	Val	Gln	Ala	
182	65					70					75				80		

183

184	GAA	GAC	CTG	GCA	GTT	TAT	TTC	TGT	CAG	CAG	GAT	TAT	AGC	TCT	CCG	TAC	288
185	Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys	Gln	Gln	Asp	Tyr	Ser	Ser	Pro	Tyr	
186					85					90				95			

187

188	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAG	ATC							318
189	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile							
190			100					105									

191

192

193 (2) INFORMATION FOR SEQ ID NO:4:

194

195 (i) SEQUENCE CHARACTERISTICS:

196 (A) LENGTH: 106 amino acids

197 (B) TYPE: amino acid

198 (D) TOPOLOGY: linear

199

200 (ii) MOLECULE TYPE: protein

201

202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

203

204	Ser	Ile	Val	Met	Thr	Gln	Thr	Pro	Lys	Phe	Leu	Leu	Val	Ser	Ala	Gly	
205	1				5					10					15		

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206
207 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
208 20 25 30
209
210 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
211 35 40 45
212
213 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
214 50 55 60
215
216 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
217 65 70 75 80
218
219 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
220 85 90 95
221
222 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
223 100 105
224
225

SEQUENCE VERIFICATION REPORT
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